

#4



SEQUENCE LISTING

<110> Arnaut, Greta
Boets, Anne
Vanneste, Stijn
Van Rie, Jeroen
Van Houdt, Sara

<120> Novel Bacillus thuringiensis insecticidal proteins

<130> 58764.000036

<140> US 10/040,906

<141> 2002-01-09

<160> 9

<170> PatentIn version 3.1

<210> 1

<211> 1899

<212> DNA

<213> Bacillus thuringiensis

<220>

<221> CDS

<222> (1) .. (1896)

<223>

<400> 1

atg aat aat gta tta aat aac gga aga act act att tgt gat gcg tat	48
Met Asn Asn Val Leu Asn Asn Gly Arg Thr Thr Ile Cys Asp Ala Tyr	
1 5 10 15	
aat gta gtg gcc cat gat cca ttt agt ttt gag cat aaa tca tta gat	96
Asn Val Val Ala His Asp Pro Phe Ser Phe Glu His Lys Ser Leu Asp	
20 25 30	
acc atc cga aaa gaa tgg atg gag tgg aaa aga aca gat cat agt tta	144
Thr Ile Arg Lys Glu Trp Met Glu Trp Lys Arg Thr Asp His Ser Leu	
35 40 45	
tat gta gct cct ata gtc gga act gtt tct agc ttt ctg cta aag aag	192
Tyr Val Ala Pro Ile Val Gly Thr Val Ser Ser Phe Leu Leu Lys Lys	
50 55 60	
gtg ggg agt ctt att gga aaa agg ata ttg agt gaa tta tgg ggg tta	240
Val Gly Ser Leu Ile Gly Lys Arg Ile Leu Ser Glu Leu Trp Gly Leu	
65 70 75 80	
ata ttt cct agt ggt agc aca aat cta atg caa gat att tta agg gag	288
Ile Phe Pro Ser Gly Ser Thr Asn Leu Met Gln Asp Ile Leu Arg Glu	
85 90 95	
aca gaa caa ttc cta aat caa aga ctt aat aca gac act ctt gcc cgt	336
Thr Glu Gln Phe Leu Asn Gln Arg Leu Asn Thr Asp Thr Leu Ala Arg	
100 105 110	
gta aat gcg gaa ttg gaa ggg ctg caa gcg aat ata agg gag ttt aat	384
Val Asn Ala Glu Leu Glu Gly Leu Gln Ala Asn Ile Arg Glu Phe Asn	

115	120	125	
caa caa gta gat aat ttt tta aat cct act caa aac cct gtt cct tta Gln Gln Val Asp Asn Phe Leu Asn Pro Thr Gln Asn Pro Val Pro Leu 130 135 140			432
tca ata act tct tca gtt aat aca atg cag caa tta ttt cta aat aga Ser Ile Thr Ser Ser Val Asn Thr Met Gln Gln Leu Phe Leu Asn Arg 145 150 155 160			480
tta ccc cag ttc cgt gtg caa gga tac caa ctg tta tta tta cct tta Leu Pro Gln Phe Arg Val Gln Gly Tyr Gln Leu Leu Leu Leu Pro Leu 165 170 175			528
ttt gca cag gca gcc aat atg cat ctt tct ttt att aga gat gtt gtt Phe Ala Gln Ala Ala Asn Met His Leu Ser Phe Ile Arg Asp Val Val 180 185 190			576
ctc aat gca gat gaa tgg gga att tca gca gca aca tta cgt acg tat Leu Asn Ala Asp Glu Trp Gly Ile Ser Ala Ala Thr Leu Arg Thr Tyr 195 200 205			624
caa aat tat ctg aaa aat tat aca aca gag tac tct aat tat tgt ata Gln Asn Tyr Leu Lys Asn Tyr Thr Thr Glu Tyr Ser Asn Tyr Cys Ile 210 215 220			672
aat acg tat caa act gcg ttt aga ggt tta aac acc cgt tta cac gat Asn Thr Tyr Gln Thr Ala Phe Arg Gly Leu Asn Thr Arg Leu His Asp 225 230 235 240			720
atg tta gaa ttt aga aca tat atg ttt tta aat gta ttt gaa tat gta Met Leu Glu Phe Arg Thr Tyr Met Phe Leu Asn Val Phe Glu Tyr Val 245 250 255			768
tct atc tgg tcg ttg ttt aaa tat caa agc ctt cta gta tct tct ggc Ser Ile Trp Ser Leu Phe Lys Tyr Gln Ser Leu Leu Val Ser Ser Gly 260 265 270			816
gct aat tta tat gca agc ggt agt gga cca cag cag act caa tca ttt Ala Asn Leu Tyr Ala Ser Gly Ser Gly Pro Gln Gln Thr Gln Ser Phe 275 280 285			864
act tca caa gac tgg cca ttt tta tat tct ctt ttc caa gtt aat tca Thr Ser Gln Asp Trp Pro Phe Leu Tyr Ser Leu Phe Gln Val Asn Ser 290 295 300			912
aat tat gtg tta aat ggc ttt agt ggc gct aga ctt acg cag act ttc Asn Tyr Val Leu Asn Gly Phe Ser Gly Ala Arg Leu Thr Gln Thr Phe 305 310 315 320			960
cct aat att ggt ggt tta cct ggt act act aca act cac gca ttg ctt Pro Asn Ile Gly Gly Leu Pro Gly Thr Thr Thr Thr His Ala Leu Leu 325 330 335			1008
gcg gca agg gtc aat tac agt gga gga gtt tcg tct ggt gat ata ggc Ala Ala Arg Val Asn Tyr Ser Gly Gly Val Ser Ser Gly Asp Ile Gly 340 345 350			1056
gct gtg ttt aat caa aat ttt agt tgt agc aca ttt ctc cca cct ttg Ala Val Phe Asn Gln Asn Phe Ser Cys Ser Thr Phe Leu Pro Pro Leu 355 360 365			1104

tta aca cca ttt gtt agg agt tgg cta gat tca ggt tca gat cga ggg Leu Thr Pro Phe Val Arg Ser Trp Leu Asp Ser Gly Ser Asp Arg Gly 370 375 380	1152
ggt gtt aat acc gtt aca aat tgg caa aca gaa tcg ttt gag tca act Gly Val Asn Thr Val Thr Asn Trp Gln Thr Glu Ser Phe Glu Ser Thr 385 390 395 400	1200
tta ggt tta agg tgt ggt gct ttt aca gct cgt ggt aat tca aac tat Leu Gly Leu Arg Cys Gly Ala Phe Thr Ala Arg Gly Asn Ser Asn Tyr 405 410 415	1248
ttc cca gat tat ttt atc cgt aat att tca gga gtt cct tta gtt gtt Phe Pro Asp Tyr Phe Ile Arg Asn Ile Ser Gly Val Pro Leu Val Val 420 425 430	1296
aga aat gaa gat tta aga aga ccg tta cac tat aat gaa ata aga aat Arg Asn Glu Asp Leu Arg Arg Pro Leu His Tyr Asn Glu Ile Arg Asn 435 440 445	1344
ata gaa agt cct tca gga aca cct ggt gga tta cga gct tat atg gta Ile Glu Ser Pro Ser Gly Thr Pro Gly Gly Leu Arg Ala Tyr Met Val 450 455 460	1392
tct gtg cat aat aga aaa aat aat atc tat gcc gtg cat gaa aat ggt Ser Val His Asn Arg Lys Asn Asn Ile Tyr Ala Val His Glu Asn Gly 465 470 475 480	1440
act atg att cat tta gcg ccg gaa gat tat aca gga ttc acc ata tcg Thr Met Ile His Leu Ala Pro Glu Asp Tyr Thr Gly Phe Thr Ile Ser 485 490 495	1488
ccg ata cat gca act caa gtg aat aat caa acg cga aca ttt att tct Pro Ile His Ala Thr Gln Val Asn Asn Gln Thr Arg Thr Phe Ile Ser 500 505 510	1536
gaa aaa ttt gga aat caa ggt gat tcc tta aga ttt gaa caa agc aac Glu Lys Phe Gly Asn Gln Gly Asp Ser Leu Arg Phe Glu Gln Ser Asn 515 520 525	1584
acg aca gca cgt tat aca ctt aga gga aat gga aat agt tac aat ctt Thr Thr Ala Arg Tyr Thr Leu Arg Gly Asn Gly Asn Ser Tyr Asn Leu 530 535 540	1632
tat tta aga gta tct tca cta gga aat tcc act att cga gtt act ata Tyr Leu Arg Val Ser Ser Leu Gly Asn Ser Thr Ile Arg Val Thr Ile 545 550 555 560	1680
aac ggt agg gtt tat act gct tca aat gtt aat act act aca aat aac Asn Gly Arg Val Tyr Thr Ala Ser Asn Val Asn Thr Thr Thr Asn Asn 565 570 575	1728
gat gga gtt aat gat aat ggc gct cgt ttt tta gat att aat atg ggt Asp Gly Val Asn Asp Asn Gly Ala Arg Phe Leu Asp Ile Asn Met Gly 580 585 590	1776
aat gta gta gca agt gat aat act aat gta ccg tta gat ata aat gtg Asn Val Val Ala Ser Asp Asn Thr Asn Val Pro Leu Asp Ile Asn Val 595 600 605	1824

aca ttt aac tcc ggt act caa ttt gag ctt atg aat att atg ttt gtt 1872
 Thr Phe Asn Ser Gly Thr Gln Phe Glu Leu Met Asn Ile Met Phe Val
 610 615 620

cca act aat ctt cca cca ata tat taa 1899
 Pro Thr Asn Leu Pro Pro Ile Tyr
 625 630

<210> 2
 <211> 632
 <212> PRT
 <213> Bacillus thuringiensis

<400> 2

Met Asn Asn Val Leu Asn Asn Gly Arg Thr Thr Ile Cys Asp Ala Tyr
 1 5 10 15

Asn Val Val Ala His Asp Pro Phe Ser Phe Glu His Lys Ser Leu Asp
 20 25 30

Thr Ile Arg Lys Glu Trp Met Glu Trp Lys Arg Thr Asp His Ser Leu
 35 40 45

Tyr Val Ala Pro Ile Val Gly Thr Val Ser Ser Phe Leu Leu Lys Lys
 50 55 60

Val Gly Ser Leu Ile Gly Lys Arg Ile Leu Ser Glu Leu Trp Gly Leu
 65 70 75 80

Ile Phe Pro Ser Gly Ser Thr Asn Leu Met Gln Asp Ile Leu Arg Glu
 85 90 95

Thr Glu Gln Phe Leu Asn Gln Arg Leu Asn Thr Asp Thr Leu Ala Arg
 100 105 110

Val Asn Ala Glu Leu Glu Gly Leu Gln Ala Asn Ile Arg Glu Phe Asn
 115 120 125

Gln Gln Val Asp Asn Phe Leu Asn Pro Thr Gln Asn Pro Val Pro Leu
 130 135 140

Ser Ile Thr Ser Ser Val Asn Thr Met Gln Gln Leu Phe Leu Asn Arg
 145 150 155 160

Leu Pro Gln Phe Arg Val Gln Gly Tyr Gln Leu Leu Leu Leu Pro Leu
 165 170 175

Phe Ala Gln Ala Ala Asn Met His Leu Ser Phe Ile Arg Asp Val Val

180	185	190
Leu Asn Ala Asp Glu Trp Gly Ile Ser Ala Ala Thr Leu Arg Thr Tyr 195 200 205		
Gln Asn Tyr Leu Lys Asn Tyr Thr Thr Glu Tyr Ser Asn Tyr Cys Ile 210 215 220		
Asn Thr Tyr Gln Thr Ala Phe Arg Gly Leu Asn Thr Arg Leu His Asp 225 230 235 240		
Met Leu Glu Phe Arg Thr Tyr Met Phe Leu Asn Val Phe Glu Tyr Val 245 250 255		
Ser Ile Trp Ser Leu Phe Lys Tyr Gln Ser Leu Leu Val Ser Ser Gly 260 265 270		
Ala Asn Leu Tyr Ala Ser Gly Ser Gly Pro Gln Gln Thr Gln Ser Phe 275 280 285		
Thr Ser Gln Asp Trp Pro Phe Leu Tyr Ser Leu Phe Gln Val Asn Ser 290 295 300		
Asn Tyr Val Leu Asn Gly Phe Ser Gly Ala Arg Leu Thr Gln Thr Phe 305 310 315 320		
Pro Asn Ile Gly Gly Leu Pro Gly Thr Thr Thr Thr His Ala Leu Leu 325 330 335		
Ala Ala Arg Val Asn Tyr Ser Gly Gly Val Ser Ser Gly Asp Ile Gly 340 345 350		
Ala Val Phe Asn Gln Asn Phe Ser Cys Ser Thr Phe Leu Pro Pro Leu 355 360 365		
Leu Thr Pro Phe Val Arg Ser Trp Leu Asp Ser Gly Ser Asp Arg Gly 370 375 380		
Gly Val Asn Thr Val Thr Asn Trp Gln Thr Glu Ser Phe Glu Ser Thr 385 390 395 400		
Leu Gly Leu Arg Cys Gly Ala Phe Thr Ala Arg Gly Asn Ser Asn Tyr 405 410 415		
Phe Pro Asp Tyr Phe Ile Arg Asn Ile Ser Gly Val Pro Leu Val Val 420 425 430		

Arg Asn Glu Asp Leu Arg Arg Pro Leu His Tyr Asn Glu Ile Arg Asn
 435 440 445
 Ile Glu Ser Pro Ser Gly Thr Pro Gly Gly Leu Arg Ala Tyr Met Val
 450 455 460
 Ser Val His Asn Arg Lys Asn Asn Ile Tyr Ala Val His Glu Asn Gly
 465 470 475 480
 Thr Met Ile His Leu Ala Pro Glu Asp Tyr Thr Gly Phe Thr Ile Ser
 485 490 495
 Pro Ile His Ala Thr Gln Val Asn Asn Gln Thr Arg Thr Phe Ile Ser
 500 505 510
 Glu Lys Phe Gly Asn Gln Gly Asp Ser Leu Arg Phe Glu Gln Ser Asn
 515 520 525
 Thr Thr Ala Arg Tyr Thr Leu Arg Gly Asn Gly Asn Ser Tyr Asn Leu
 530 535 540
 Tyr Leu Arg Val Ser Ser Leu Gly Asn Ser Thr Ile Arg Val Thr Ile
 545 550 555 560
 Asn Gly Arg Val Tyr Thr Ala Ser Asn Val Asn Thr Thr Thr Asn Asn
 565 570 575
 Asp Gly Val Asn Asp Asn Gly Ala Arg Phe Leu Asp Ile Asn Met Gly
 580 585 590
 Asn Val Val Ala Ser Asp Asn Thr Asn Val Pro Leu Asp Ile Asn Val
 595 600 605
 Thr Phe Asn Ser Gly Thr Gln Phe Glu Leu Met Asn Ile Met Phe Val
 610 615 620
 Pro Thr Asn Leu Pro Pro Ile Tyr
 625 630

<210> 3
 <211> 1899
 <212> DNA
 <213> Bacillus thuringiensis

<220>
 <221> CDS

<222> (1) .. (1896)
<223>

<400> 3

atg aat agt gta ttg aat agc gga aga act act att tgt gat gcg tat	48
Met Asn Ser Val Leu Asn Ser Gly Arg Thr Thr Ile Cys Asp Ala Tyr	
1 5 10 15	
aat gta gtg gct cat gat cca ttt agt ttt caa cat aaa tca tta gat	96
Asn Val Val Ala His Asp Pro Phe Ser Phe Gln His Lys Ser Leu Asp	
20 25 30	
acc ata caa gaa gaa tgg atg gag tgg aaa aaa gat aat cat agt tta	144
Thr Ile Gln Glu Glu Trp Met Glu Trp Lys Lys Asp Asn His Ser Leu	
35 40 45	
tat gta gat cct att gtt gga act gtg gct agt ttt ctt tta aag aaa	192
Tyr Val Asp Pro Ile Val Gly Thr Val Ala Ser Phe Leu Leu Lys Lys	
50 55 60	
gtg ggg agt ctt gtt gga aaa aga ata ctg agt gag tta cgg aat tta	240
Val Gly Ser Leu Val Gly Lys Arg Ile Leu Ser Glu Leu Arg Asn Leu	
65 70 75 80	
ata ttt cct agt ggc agt aca aat cta atg caa gat att tta aga gag	288
Ile Phe Pro Ser Gly Ser Thr Asn Leu Met Gln Asp Ile Leu Arg Glu	
85 90 95	
aca gaa aaa ttc ctg aat caa aga ctt aat aca gac act ctt gcc cgt	336
Thr Glu Lys Phe Leu Asn Gln Arg Leu Asn Thr Asp Thr Leu Ala Arg	
100 105 110	
gta aat gcg gaa ttg aca ggg ctg caa gca aat gta gaa gag ttt aat	384
Val Asn Ala Glu Leu Thr Gly Leu Gln Ala Asn Val Glu Glu Phe Asn	
115 120 125	
cga caa gta gat aat ttt ttg aac cct aac cga aat gct gtt cct tta	432
Arg Gln Val Asp Asn Phe Leu Asn Pro Asn Arg Asn Ala Val Pro Leu	
130 135 140	
tca ata act tct tca gtt aat aca atg cag caa tta ttt cta aat aga	480
Ser Ile Thr Ser Ser Val Asn Thr Met Gln Gln Leu Phe Leu Asn Arg	
145 150 155 160	
tta acc cag ttc cag atg caa gga tac caa ttg tta tta tta cct tta	528
Leu Thr Gln Phe Gln Met Gln Gly Tyr Gln Leu Leu Leu Leu Pro Leu	
165 170 175	
ttt gca cag gca gcc aat tta cat ctt tct ttt att aga gat gtt att	576
Phe Ala Gln Ala Ala Asn Leu His Leu Ser Phe Ile Arg Asp Val Ile	
180 185 190	
ctt aat gca gac gaa tgg gga att tca gca gca aca tta cgt acg tat	624
Leu Asn Ala Asp Glu Trp Gly Ile Ser Ala Ala Thr Leu Arg Thr Tyr	
195 200 205	
caa aat cac ctg aga aat tat aca aga gat tac tct aat tat tgt ata	672
Gln Asn His Leu Arg Asn Tyr Thr Arg Asp Tyr Ser Asn Tyr Cys Ile	
210 215 220	

aat acg tat caa act gcg ttt aga ggt tta aac acc cgt tta cac gat Asn Thr Tyr Gln Thr Ala Phe Arg Gly Leu Asn Thr Arg Leu His Asp 225 230 235 240	720
atg tta gaa ttt aga aca tat atg ttt tta aat gta ttt gag tat gta Met Leu Glu Phe Arg Thr Tyr Met Phe Leu Asn Val Phe Glu Tyr Val 245 250 255	768
tct atc tgg tcg ttg ttt aaa tat caa agc ctt cta gtc tct tct ggc Ser Ile Trp Ser Leu Phe Lys Tyr Gln Ser Leu Leu Val Ser Ser Gly 260 265 270	816
gct aat tta tat gca agt ggt agt gga cca cag cag acc caa tca ttt Ala Asn Leu Tyr Ala Ser Gly Ser Gly Pro Gln Gln Thr Gln Ser Phe 275 280 285	864
act tca caa gac tgg cca ttt tta tat tct ctt ttc caa gtt aat tca Thr Ser Gln Asp Trp Pro Phe Leu Tyr Ser Leu Phe Gln Val Asn Ser 290 295 300	912
aat tat gtg tta aat ggc ttt agt ggc gct aga ctt acg cag act ttc Asn Tyr Val Leu Asn Gly Phe Ser Gly Ala Arg Leu Thr Gln Thr Phe 305 310 315 320	960
cct aat att gtt ggt tta cct ggt act act aca act cac gca ttg ctt Pro Asn Ile Val Gly Leu Pro Gly Thr Thr Thr Thr His Ala Leu Leu 325 330 335	1008
gct gca agg gtc aat tac agt gga gga gtt tcg tct ggt gat ata ggc Ala Ala Arg Val Asn Tyr Ser Gly Gly Val Ser Ser Gly Asp Ile Gly 340 345 350	1056
gct gtg ttt aat caa aat ttt agt tgt agc aca ttt ctc cca cct ttg Ala Val Phe Asn Gln Asn Phe Ser Cys Ser Thr Phe Leu Pro Pro Leu 355 360 365	1104
tta aca cca ttt gtt agg agt tgg cta gat tca ggt tca gat cgg ggg Leu Thr Pro Phe Val Arg Ser Trp Leu Asp Ser Gly Ser Asp Arg Gly 370 375 380	1152
ggg atc aat acc gtt acc aat tgg caa aca gaa tcc ttt gag aca act Gly Ile Asn Thr Val Thr Asn Trp Gln Thr Glu Ser Phe Glu Thr Thr 385 390 395 400	1200
tta ggt tta agg agt ggt gct ttt aca gct cga ggt aat tca aac tat Leu Gly Leu Arg Ser Gly Ala Phe Thr Ala Arg Gly Asn Ser Asn Tyr 405 410 415	1248
ttc cca gat tat ttt atc cgt aat att tcc gga gtt cct tta gtt gtt Phe Pro Asp Tyr Phe Ile Arg Asn Ile Ser Gly Val Pro Leu Val Val 420 425 430	1296
aga aat gaa gat tta aga aga ccg tta cac tat aat caa ata aga aat Arg Asn Glu Asp Leu Arg Arg Pro Leu His Tyr Asn Gln Ile Arg Asn 435 440 445	1344
ata gaa agt cct tca gga aca cct ggt gga tta cga gct tat atg gta Ile Glu Ser Pro Ser Gly Thr Pro Gly Gly Leu Arg Ala Tyr Met Val 450 455 460	1392
tct gtg cat aac aga aaa aat aat atc tat gcc gtt cat gaa aat ggt	1440

Ser	Val	His	Asn	Arg	Lys	Asn	Asn	Ile	Tyr	Ala	Val	His	Glu	Asn	Gly	
465					470					475					480	
act	atg	att	cat	tta	gcg	ccg	gaa	gat	tat	aca	gga	ttt	act	ata	tcg	1488
Thr	Met	Ile	His	Leu	Ala	Pro	Glu	Asp	Tyr	Thr	Gly	Phe	Thr	Ile	Ser	
				485					490					495		
ccg	ata	cat	gca	act	caa	gtg	aat	aat	caa	acg	cga	aca	ttt	att	tct	1536
Pro	Ile	His	Ala	Thr	Gln	Val	Asn	Asn	Gln	Thr	Arg	Thr	Phe	Ile	Ser	
			500					505					510			
gaa	aaa	ttt	gga	aat	caa	ggt	gat	tcc	tta	aga	ttt	gaa	caa	agc	aac	1584
Glu	Lys	Phe	Gly	Asn	Gln	Gly	Asp	Ser	Leu	Arg	Phe	Glu	Gln	Ser	Asn	
		515					520					525				
acg	aca	gct	cgt	tat	aca	ctt	aga	ggg	aat	gga	aat	agt	tac	aat	ctt	1632
Thr	Thr	Ala	Arg	Tyr	Thr	Leu	Arg	Gly	Asn	Gly	Asn	Ser	Tyr	Asn	Leu	
		530				535					540					
tat	tta	aga	gta	tct	tca	ata	gga	aat	tcc	act	att	cga	gtt	act	ata	1680
Tyr	Leu	Arg	Val	Ser	Ser	Ile	Gly	Asn	Ser	Thr	Ile	Arg	Val	Thr	Ile	
545					550				555						560	
aac	ggt	aga	gtt	tat	act	gct	tca	aat	gtt	aat	act	act	aca	aat	aac	1728
Asn	Gly	Arg	Val	Tyr	Thr	Ala	Ser	Asn	Val	Asn	Thr	Thr	Thr	Asn	Asn	
				565				570						575		
gat	gga	gtt	aat	gat	aat	gga	gct	cgt	ttt	tca	gat	att	aat	att	ggt	1776
Asp	Gly	Val	Asn	Asp	Asn	Gly	Ala	Arg	Phe	Ser	Asp	Ile	Asn	Ile	Gly	
			580					585					590			
aat	gta	gta	gca	agt	gat	aat	act	aat	gta	ccg	tta	gat	ata	aac	gtg	1824
Asn	Val	Val	Ala	Ser	Asp	Asn	Thr	Asn	Val	Pro	Leu	Asp	Ile	Asn	Val	
			595				600					605				
aca	tta	aat	tct	ggt	act	caa	ttt	gag	ctt	atg	aat	att	atg	ttt	gtt	1872
Thr	Leu	Asn	Ser	Gly	Thr	Gln	Phe	Glu	Leu	Met	Asn	Ile	Met	Phe	Val	
		610				615					620					
cca	act	aat	atc	tca	cca	ctt	tat	taa								1899
Pro	Thr	Asn	Ile	Ser	Pro	Leu	Tyr									
625					630											

<210> 4
 <211> 632
 <212> PRT
 <213> Bacillus thuringiensis

<400> 4

Met	Asn	Ser	Val	Leu	Asn	Ser	Gly	Arg	Thr	Thr	Ile	Cys	Asp	Ala	Tyr
1				5					10					15	
Asn	Val	Val	Ala	His	Asp	Pro	Phe	Ser	Phe	Gln	His	Lys	Ser	Leu	Asp
			20					25					30		
Thr	Ile	Gln	Glu	Glu	Trp	Met	Glu	Trp	Lys	Lys	Asp	Asn	His	Ser	Leu
		35					40					45			

Tyr Val Asp Pro Ile Val Gly Thr Val Ala Ser Phe Leu Leu Lys Lys
50 55 60

Val Gly Ser Leu Val Gly Lys Arg Ile Leu Ser Glu Leu Arg Asn Leu
65 70 75 80

Ile Phe Pro Ser Gly Ser Thr Asn Leu Met Gln Asp Ile Leu Arg Glu
85 90 95

Thr Glu Lys Phe Leu Asn Gln Arg Leu Asn Thr Asp Thr Leu Ala Arg
100 105 110

Val Asn Ala Glu Leu Thr Gly Leu Gln Ala Asn Val Glu Glu Phe Asn
115 120 125

Arg Gln Val Asp Asn Phe Leu Asn Pro Asn Arg Asn Ala Val Pro Leu
130 135 140

Ser Ile Thr Ser Ser Val Asn Thr Met Gln Gln Leu Phe Leu Asn Arg
145 150 155 160

Leu Thr Gln Phe Gln Met Gln Gly Tyr Gln Leu Leu Leu Leu Pro Leu
165 170 175

Phe Ala Gln Ala Ala Asn Leu His Leu Ser Phe Ile Arg Asp Val Ile
180 185 190

Leu Asn Ala Asp Glu Trp Gly Ile Ser Ala Ala Thr Leu Arg Thr Tyr
195 200 205

Gln Asn His Leu Arg Asn Tyr Thr Arg Asp Tyr Ser Asn Tyr Cys Ile
210 215 220

Asn Thr Tyr Gln Thr Ala Phe Arg Gly Leu Asn Thr Arg Leu His Asp
225 230 235 240

Met Leu Glu Phe Arg Thr Tyr Met Phe Leu Asn Val Phe Glu Tyr Val
245 250 255

Ser Ile Trp Ser Leu Phe Lys Tyr Gln Ser Leu Leu Val Ser Ser Gly
260 265 270

Ala Asn Leu Tyr Ala Ser Gly Ser Gly Pro Gln Gln Thr Gln Ser Phe
275 280 285

Thr Ser Gln Asp Trp Pro Phe Leu Tyr Ser Leu Phe Gln Val Asn Ser
290 295 300

Asn Tyr Val Leu Asn Gly Phe Ser Gly Ala Arg Leu Thr Gln Thr Phe
305 310 315 320

Pro Asn Ile Val Gly Leu Pro Gly Thr Thr Thr Thr His Ala Leu Leu
325 330 335

Ala Ala Arg Val Asn Tyr Ser Gly Gly Val Ser Ser Gly Asp Ile Gly
340 345 350

Ala Val Phe Asn Gln Asn Phe Ser Cys Ser Thr Phe Leu Pro Pro Leu
355 360 365

Leu Thr Pro Phe Val Arg Ser Trp Leu Asp Ser Gly Ser Asp Arg Gly
370 375 380

Gly Ile Asn Thr Val Thr Asn Trp Gln Thr Glu Ser Phe Glu Thr Thr
385 390 395 400

Leu Gly Leu Arg Ser Gly Ala Phe Thr Ala Arg Gly Asn Ser Asn Tyr
405 410 415

Phe Pro Asp Tyr Phe Ile Arg Asn Ile Ser Gly Val Pro Leu Val Val
420 425 430

Arg Asn Glu Asp Leu Arg Arg Pro Leu His Tyr Asn Gln Ile Arg Asn
435 440 445

Ile Glu Ser Pro Ser Gly Thr Pro Gly Gly Leu Arg Ala Tyr Met Val
450 455 460

Ser Val His Asn Arg Lys Asn Asn Ile Tyr Ala Val His Glu Asn Gly
465 470 475 480

Thr Met Ile His Leu Ala Pro Glu Asp Tyr Thr Gly Phe Thr Ile Ser
485 490 495

Pro Ile His Ala Thr Gln Val Asn Asn Gln Thr Arg Thr Phe Ile Ser
500 505 510

Glu Lys Phe Gly Asn Gln Gly Asp Ser Leu Arg Phe Glu Gln Ser Asn
515 520 525

Thr Thr Ala Arg Tyr Thr Leu Arg Gly Asn Gly Asn Ser Tyr Asn Leu
530 535 540

Tyr Leu Arg Val Ser Ser Ile Gly Asn Ser Thr Ile Arg Val Thr Ile
545 550 555 560

Asn Gly Arg Val Tyr Thr Ala Ser Asn Val Asn Thr Thr Thr Asn Asn
565 570 575

Asp Gly Val Asn Asp Asn Gly Ala Arg Phe Ser Asp Ile Asn Ile Gly
580 585 590

Asn Val Val Ala Ser Asp Asn Thr Asn Val Pro Leu Asp Ile Asn Val
595 600 605

Thr Leu Asn Ser Gly Thr Gln Phe Glu Leu Met Asn Ile Met Phe Val
610 615 620

Pro Thr Asn Ile Ser Pro Leu Tyr
625 630

<210> 5
<211> 1884
<212> DNA
<213> Bacillus thuringiensis

<220>
<221> CDS
<222> (1)..(1881)
<223>

<400> 5
atg aat aat gta ttg aat agc gaa aga act act aag tgt ggt gcg tat 48
Met Asn Asn Val Leu Asn Ser Glu Arg Thr Thr Lys Cys Gly Ala Tyr
1 5 10 15
aac gta gtg gct cat gat cca ttc agt ttt gaa cat aaa tca tta gat 96
Asn Val Val Ala His Asp Pro Phe Ser Phe Glu His Lys Ser Leu Asp
20 25 30
acc ata caa aaa gaa tgg atg gag tgg aaa aga act gat cat agt tta 144
Thr Ile Gln Lys Glu Trp Met Glu Trp Lys Arg Thr Asp His Ser Leu
35 40 45
tat gta tct cct att gta gga act ata gcc agt ttt ctg tta aag aaa 192
Tyr Val Ser Pro Ile Val Gly Thr Ile Ala Ser Phe Leu Leu Lys Lys
50 55 60
ata gga ggg ctt ata gga aaa aga ata tta agt gag tta aag aat tta 240
Ile Gly Gly Leu Ile Gly Lys Arg Ile Leu Ser Glu Leu Lys Asn Leu
65 70 75 80
att ttt cct agt ggt agt ata gaa tca atg caa gat att tta aga ggg 288

Ile	Phe	Pro	Ser	Gly	Ser	Ile	Glu	Ser	Met	Gln	Asp	Ile	Leu	Arg	Gly		
				85					90					95			
gca	gaa	caa	ttt	cta	aat	caa	aga	ctt	gat	gca	gac	acc	ttt	agt	cgt	336	
Ala	Glu	Gln	Phe	Leu	Asn	Gln	Arg	Leu	Asp	Ala	Asp	Thr	Phe	Ser	Arg		
			100					105					110				
gta	gaa	gca	gaa	ttg	aga	ggg	ctt	caa	gca	aat	gta	gag	gaa	ttt	aat	384	
Val	Glu	Ala	Glu	Leu	Arg	Gly	Leu	Gln	Ala	Asn	Val	Glu	Glu	Phe	Asn		
			115				120					125					
cga	caa	gtg	gac	aat	ttt	tta	aac	cca	aat	caa	aac	cct	gcc	cct	tta	432	
Arg	Gln	Val	Asp	Asn	Phe	Leu	Asn	Pro	Asn	Gln	Asn	Pro	Ala	Pro	Leu		
			130			135					140						
gca	ata	att	gat	tcg	gtt	aat	aca	ttg	caa	caa	tta	ttc	cta	agt	aga	480	
Ala	Ile	Ile	Asp	Ser	Val	Asn	Thr	Leu	Gln	Gln	Leu	Phe	Leu	Ser	Arg		
					150				155						160		
tta	ccc	cag	ttc	cag	ata	caa	cgc	tat	cag	cta	tta	tta	tta	cct	tta	528	
Leu	Pro	Gln	Phe	Gln	Ile	Gln	Arg	Tyr	Gln	Leu	Leu	Leu	Leu	Pro	Leu		
				165				170						175			
ttt	gca	caa	gca	gcc	aat	tta	cac	ctt	tct	ttt	att	aga	gac	gtt	att	576	
Phe	Ala	Gln	Ala	Ala	Asn	Leu	His	Leu	Ser	Phe	Ile	Arg	Asp	Val	Ile		
			180					185					190				
ctt	aat	gca	gat	gaa	tgg	gga	ata	cca	gct	gca	acg	gtg	cgc	aca	tat	624	
Leu	Asn	Ala	Asp	Glu	Trp	Gly	Ile	Pro	Ala	Ala	Thr	Val	Arg	Thr	Tyr		
			195			200						205					
aga	gag	cac	cta	caa	aga	tat	aca	cgc	gaa	tac	tcc	aat	tat	tgt	ata	672	
Arg	Glu	His	Leu	Gln	Arg	Tyr	Thr	Arg	Glu	Tyr	Ser	Asn	Tyr	Cys	Ile		
			210			215					220						
aat	acg	tat	caa	act	gcg	ttt	aga	ggg	tta	aat	gcc	act	tta	cac	gat	720	
Asn	Thr	Tyr	Gln	Thr	Ala	Phe	Arg	Gly	Leu	Asn	Ala	Thr	Leu	His	Asp		
					230					235					240		
ttt	cta	gaa	ttt	aga	aca	tat	atg	ttt	tta	aat	gta	tta	gac	tat	gta	768	
Phe	Leu	Glu	Phe	Arg	Thr	Tyr	Met	Phe	Leu	Asn	Val	Leu	Asp	Tyr	Val		
				245				250						255			
tct	atc	tgg	tcg	ttg	ttt	aaa	tat	cag	agc	ctt	ctg	gta	tcc	tct	ggc	816	
Ser	Ile	Trp	Ser	Leu	Phe	Lys	Tyr	Gln	Ser	Leu	Leu	Val	Ser	Ser	Gly		
			260					265					270				
gct	aat	tta	tat	gcg	agt	ggt	agt	gga	gta	aca	aat	aga	caa	tca	ttt	864	
Ala	Asn	Leu	Tyr	Ala	Ser	Gly	Ser	Gly	Val	Thr	Asn	Arg	Gln	Ser	Phe		
			275			280						285					
act	gca	caa	gac	tgg	cca	ttt	tta	aat	tct	ctt	ttc	caa	gtt	aat	caa	912	
Thr	Ala	Gln	Asp	Trp	Pro	Phe	Leu	Asn	Ser	Leu	Phe	Gln	Val	Asn	Gln		
			290			295					300						
aat	tat	gta	tta	aca	ggt	atg	aat	ggt	tat	agg	tat	act	tta	agt	tct	960	
Asn	Tyr	Val	Leu	Thr	Gly	Met	Asn	Gly	Tyr	Arg	Tyr	Thr	Leu	Ser	Ser		
				310				315						320			
gtt	ttt	ggt	aca	aat	caa	aca	ata	cat	tct	gtt	agg	agt	aat	tat	agg	1008	
Val	Phe	Gly	Thr	Asn	Gln	Thr	Ile	His	Ser	Val	Arg	Ser	Asn	Tyr	Arg		

325	330	335	
ggc ggg gtt tca tct ggt tac att gga gtt aat ctt agt gaa ggt gac Gly Gly Val Ser Ser Gly Tyr Ile Gly Val Asn Leu Ser Glu Gly Asp 340 345 350			1056
caa aat ttt agt tgt agt aca ttt ttg gat cct tta gaa aca ccg ttt Gln Asn Phe Ser Cys Ser Thr Phe Leu Asp Pro Leu Glu Thr Pro Phe 355 360 365			1104
att aga agt tgg ctg gat tca ggt agc gat gat ggc ttt aat tgg agt Ile Arg Ser Trp Leu Asp Ser Gly Ser Asp Asp Gly Phe Asn Trp Ser 370 375 380			1152
aca gga gtc ttt aca aca act att ggt tta cct act tgt agc att ttt Thr Gly Val Phe Thr Thr Thr Ile Gly Leu Pro Thr Cys Ser Ile Phe 385 390 395 400			1200
tgg cct cgt ggt aac tcg aac tat ttt cca gat tat ttt ata cga aat Trp Pro Arg Gly Asn Ser Asn Tyr Phe Pro Asp Tyr Phe Ile Arg Asn 405 410 415			1248
att tct ggt gtc gtt ggt cgt ctt agg aac gaa gat tta aga aga cca Ile Ser Gly Val Val Gly Arg Leu Arg Asn Glu Asp Leu Arg Arg Pro 420 425 430			1296
cta tat ttt aat gag ata aga aat ata gta gga aat aac aat cca ccg Leu Tyr Phe Asn Glu Ile Arg Asn Ile Val Gly Asn Asn Asn Pro Pro 435 440 445			1344
gca act gga tcg tta tca gtc gcc agc cta gtc tct gtg cat aac aga Ala Thr Gly Ser Leu Ser Val Ala Ser Leu Val Ser Val His Asn Arg 450 455 460			1392
aaa aat aat att tat gct gct cat gaa aat ggt act atg att cat ttg Lys Asn Asn Ile Tyr Ala Ala His Glu Asn Gly Thr Met Ile His Leu 465 470 475 480			1440
gca ccg gaa gat tat aca ggt ttc aca atg tca cca ata cat gca act Ala Pro Glu Asp Tyr Thr Gly Phe Thr Met Ser Pro Ile His Ala Thr 485 490 495			1488
caa gta aat aat caa aca cga aca ttt att tcc gag aaa tta gga aac Gln Val Asn Asn Gln Thr Arg Thr Phe Ile Ser Glu Lys Leu Gly Asn 500 505 510			1536
caa ggt gat tcc ttg aga ttt gaa caa aca aat aca acg gct cga tac Gln Gly Asp Ser Leu Arg Phe Glu Gln Thr Asn Thr Thr Ala Arg Tyr 515 520 525			1584
aca ttt aga ggg aat gga aat agt tac aat ctt tat tta aga gta tct Thr Phe Arg Gly Asn Gly Asn Ser Tyr Asn Leu Tyr Leu Arg Val Ser 530 535 540			1632
tca cta gga aat tcc aca att cga gtt act ata aac ggt aga gtt tat Ser Leu Gly Asn Ser Thr Ile Arg Val Thr Ile Asn Gly Arg Val Tyr 545 550 555 560			1680
act gtt tca aac gtc aat act act aca aat aac gat gga gtt gtt gat Thr Val Ser Asn Val Asn Thr Thr Thr Asn Asn Asp Gly Val Val Asp 565 570 575			1728

aat ggc gct cgt ttt tca gat att aat ata ggt aat gta gtg gca agt 1776
 Asn Gly Ala Arg Phe Ser Asp Ile Asn Ile Gly Asn Val Val Ala Ser
 580 585 590

gct aat act aat ata cca tta gat ata aat gta aca ttt aac tct ggt 1824
 Ala Asn Thr Asn Ile Pro Leu Asp Ile Asn Val Thr Phe Asn Ser Gly
 595 600 605

acg caa ttt gag ctt atg aat att atg ttt gtt cca act aat att cca 1872
 Thr Gln Phe Glu Leu Met Asn Ile Met Phe Val Pro Thr Asn Ile Pro
 610 615 620

cca att tat taa 1884
 Pro Ile Tyr
 625

<210> 6
 <211> 627
 <212> PRT
 <213> Bacillus thuringiensis

<400> 6

Met Asn Asn Val Leu Asn Ser Glu Arg Thr Thr Lys Cys Gly Ala Tyr
 1 5 10 15

Asn Val Val Ala His Asp Pro Phe Ser Phe Glu His Lys Ser Leu Asp
 20 25 30

Thr Ile Gln Lys Glu Trp Met Glu Trp Lys Arg Thr Asp His Ser Leu
 35 40 45

Tyr Val Ser Pro Ile Val Gly Thr Ile Ala Ser Phe Leu Leu Lys Lys
 50 55 60

Ile Gly Gly Leu Ile Gly Lys Arg Ile Leu Ser Glu Leu Lys Asn Leu
 65 70 75 80

Ile Phe Pro Ser Gly Ser Ile Glu Ser Met Gln Asp Ile Leu Arg Gly
 85 90 95

Ala Glu Gln Phe Leu Asn Gln Arg Leu Asp Ala Asp Thr Phe Ser Arg
 100 105 110

Val Glu Ala Glu Leu Arg Gly Leu Gln Ala Asn Val Glu Glu Phe Asn
 115 120 125

Arg Gln Val Asp Asn Phe Leu Asn Pro Asn Gln Asn Pro Ala Pro Leu
 130 135 140

Ala Ile Ile Asp Ser Val Asn Thr Leu Gln Gln Leu Phe Leu Ser Arg
145 150 155 160

Leu Pro Gln Phe Gln Ile Gln Arg Tyr Gln Leu Leu Leu Leu Pro Leu
165 170 175

Phe Ala Gln Ala Ala Asn Leu His Leu Ser Phe Ile Arg Asp Val Ile
180 185 190

Leu Asn Ala Asp Glu Trp Gly Ile Pro Ala Ala Thr Val Arg Thr Tyr
195 200 205

Arg Glu His Leu Gln Arg Tyr Thr Arg Glu Tyr Ser Asn Tyr Cys Ile
210 215 220

Asn Thr Tyr Gln Thr Ala Phe Arg Gly Leu Asn Ala Thr Leu His Asp
225 230 235 240

Phe Leu Glu Phe Arg Thr Tyr Met Phe Leu Asn Val Leu Asp Tyr Val
245 250 255

Ser Ile Trp Ser Leu Phe Lys Tyr Gln Ser Leu Leu Val Ser Ser Gly
260 265 270

Ala Asn Leu Tyr Ala Ser Gly Ser Gly Val Thr Asn Arg Gln Ser Phe
275 280 285

Thr Ala Gln Asp Trp Pro Phe Leu Asn Ser Leu Phe Gln Val Asn Gln
290 295 300

Asn Tyr Val Leu Thr Gly Met Asn Gly Tyr Arg Tyr Thr Leu Ser Ser
305 310 315 320

Val Phe Gly Thr Asn Gln Thr Ile His Ser Val Arg Ser Asn Tyr Arg
325 330 335

Gly Gly Val Ser Ser Gly Tyr Ile Gly Val Asn Leu Ser Glu Gly Asp
340 345 350

Gln Asn Phe Ser Cys Ser Thr Phe Leu Asp Pro Leu Glu Thr Pro Phe
355 360 365

Ile Arg Ser Trp Leu Asp Ser Gly Ser Asp Asp Gly Phe Asn Trp Ser
370 375 380

Thr Gly Val Phe Thr Thr Thr Ile Gly Leu Pro Thr Cys Ser Ile Phe

385		390		395		400									
Trp	Pro	Arg	Gly	Asn	Ser	Asn	Tyr	Phe	Pro	Asp	Tyr	Phe	Ile	Arg	Asn
				405					410					415	
Ile	Ser	Gly	Val	Val	Gly	Arg	Leu	Arg	Asn	Glu	Asp	Leu	Arg	Arg	Pro
			420					425					430		
Leu	Tyr	Phe	Asn	Glu	Ile	Arg	Asn	Ile	Val	Gly	Asn	Asn	Asn	Pro	Pro
		435					440					445			
Ala	Thr	Gly	Ser	Leu	Ser	Val	Ala	Ser	Leu	Val	Ser	Val	His	Asn	Arg
		450				455						460			
Lys	Asn	Asn	Ile	Tyr	Ala	Ala	His	Glu	Asn	Gly	Thr	Met	Ile	His	Leu
465					470					475					480
Ala	Pro	Glu	Asp	Tyr	Thr	Gly	Phe	Thr	Met	Ser	Pro	Ile	His	Ala	Thr
				485					490					495	
Gln	Val	Asn	Asn	Gln	Thr	Arg	Thr	Phe	Ile	Ser	Glu	Lys	Leu	Gly	Asn
			500					505					510		
Gln	Gly	Asp	Ser	Leu	Arg	Phe	Glu	Gln	Thr	Asn	Thr	Thr	Ala	Arg	Tyr
		515					520					525			
Thr	Phe	Arg	Gly	Asn	Gly	Asn	Ser	Tyr	Asn	Leu	Tyr	Leu	Arg	Val	Ser
		530				535					540				
Ser	Leu	Gly	Asn	Ser	Thr	Ile	Arg	Val	Thr	Ile	Asn	Gly	Arg	Val	Tyr
545					550					555					560
Thr	Val	Ser	Asn	Val	Asn	Thr	Thr	Thr	Asn	Asn	Asp	Gly	Val	Val	Asp
				565					570					575	
Asn	Gly	Ala	Arg	Phe	Ser	Asp	Ile	Asn	Ile	Gly	Asn	Val	Val	Ala	Ser
			580					585					590		
Ala	Asn	Thr	Asn	Ile	Pro	Leu	Asp	Ile	Asn	Val	Thr	Phe	Asn	Ser	Gly
		595					600					605			
Thr	Gln	Phe	Glu	Leu	Met	Asn	Ile	Met	Phe	Val	Pro	Thr	Asn	Ile	Pro
		610				615					620				
Pro	Ile	Tyr													
625															

<210> 7
 <211> 1910
 <212> DNA
 <213> Unknown

<220>
 <223> artificial cry2Ae DNA sequence for expression in cotton
 <220>
 <221> CDS
 <222> (3)..(1901)
 <223>

<400> 7
 cc atg gct aac aac gtt ctt aac aac ggt agg act act att tgc gat 47
 Met Ala Asn Asn Val Leu Asn Asn Gly Arg Thr Thr Ile Cys Asp
 1 5 10 15
 gca tac aac gtt gtt gct cat gat cct ttc tct ttc gag cat aag tct 95
 Ala Tyr Asn Val Val Ala His Asp Pro Phe Ser Phe Glu His Lys Ser
 20 25 30
 ctt gat aca att agg aag gag tgg atg gag tgg aag agg act gat cat 143
 Leu Asp Thr Ile Arg Lys Glu Trp Met Glu Trp Lys Arg Thr Asp His
 35 40 45
 tct ctt tac gtt gct cct att gtt ggt act gtt tct tct ttc ctt ctt 191
 Ser Leu Tyr Val Ala Pro Ile Val Gly Thr Val Ser Ser Phe Leu Leu
 50 55 60
 aag aag gtt ggt tct ctt atc ggt aag agg atc ctt tct gag ctt tgg 239
 Lys Lys Val Gly Ser Leu Ile Gly Lys Arg Ile Leu Ser Glu Leu Trp
 65 70 75
 ggt ctt atc ttc cct tct ggt tct act aac ctt atg caa gat att ctt 287
 Gly Leu Ile Phe Pro Ser Gly Ser Thr Asn Leu Met Gln Asp Ile Leu
 80 85 90 95
 agg gag act gaa caa ttc ctt aac cag agg ctt aac act gat act ctt 335
 Arg Glu Thr Glu Gln Phe Leu Asn Gln Arg Leu Asn Thr Asp Thr Leu
 100 105 110
 gct agg gtt aac gct gag ctt gag ggt ctt caa gct aac att agg gaa 383
 Ala Arg Val Asn Ala Glu Leu Glu Gly Leu Gln Ala Asn Ile Arg Glu
 115 120 125
 ttc aac cag caa gtt gat aac ttc ctt aac cct act caa aac cct gtt 431
 Phe Asn Gln Gln Val Asp Asn Phe Leu Asn Pro Thr Gln Asn Pro Val
 130 135 140
 cct ctt tct att act tct tct gtt aac act atg caa caa ctt ttc ctt 479
 Pro Leu Ser Ile Thr Ser Ser Val Asn Thr Met Gln Gln Leu Phe Leu
 145 150 155
 aac agg ctt cct caa ttc agg gtt caa ggt tac caa ctt ctt ctt ctt 527
 Asn Arg Leu Pro Gln Phe Arg Val Gln Gly Tyr Gln Leu Leu Leu Leu
 160 165 170 175

cct ctt ttc gct caa gct gct aac atg cac cta agc ttc att agg gat	575
Pro Leu Phe Ala Gln Ala Ala Asn Met His Leu Ser Phe Ile Arg Asp	
180 185 190	
ggt ggt ctt aac gct gat gag tgg ggt att tct gct gct act ctt agg	623
Val Val Leu Asn Ala Asp Glu Trp Gly Ile Ser Ala Ala Thr Leu Arg	
195 200 205	
act tac caa aac tac ctt aag aac tac act act gag tac tct aac tac	671
Thr Tyr Gln Asn Tyr Leu Lys Asn Tyr Thr Thr Glu Tyr Ser Asn Tyr	
210 215 220	
tgc att aac act tac caa act gct ttc agg ggt ctt aac act agg ctt	719
Cys Ile Asn Thr Tyr Gln Thr Ala Phe Arg Gly Leu Asn Thr Arg Leu	
225 230 235	
cat gat atg ctt gag ttc agg act tac atg ttc ctt aac gtt ttc gag	767
His Asp Met Leu Glu Phe Arg Thr Tyr Met Phe Leu Asn Val Phe Glu	
240 245 250 255	
tac gtt tct att tgg tct ctt ttc aag tac cag tct ctt ctt gtt tct	815
Tyr Val Ser Ile Trp Ser Leu Phe Lys Tyr Gln Ser Leu Leu Val Ser	
260 265 270	
tct ggt gct aac ctt tac gct tct ggt tct ggt cct caa caa act caa	863
Ser Gly Ala Asn Leu Tyr Ala Ser Gly Ser Gly Pro Gln Gln Thr Gln	
275 280 285	
tct ttc act tct caa gac tgg cct ttc ctt tac tct ctt ttc caa gtt	911
Ser Phe Thr Ser Gln Asp Trp Pro Phe Leu Tyr Ser Leu Phe Gln Val	
290 295 300	
aac tct aac tac gtt ctt aac ggt ttc tct ggt gct agg ctt act caa	959
Asn Ser Asn Tyr Val Leu Asn Gly Phe Ser Gly Ala Arg Leu Thr Gln	
305 310 315	
act ttc cct aac atc ggt ggt ctt cct ggt act act act act cat gct	1007
Thr Phe Pro Asn Ile Gly Gly Leu Pro Gly Thr Thr Thr Thr His Ala	
320 325 330 335	
ctt ctt gct gct agg gtt aac tac tct ggt ggt gtt tct tct ggt gat	1055
Leu Leu Ala Ala Arg Val Asn Tyr Ser Gly Gly Val Ser Ser Gly Asp	
340 345 350	
atc ggt gct gtt ttc aac cag aac ttc tct tgc tct act ttc ctt cct	1103
Ile Gly Ala Val Phe Asn Gln Asn Phe Ser Cys Ser Thr Phe Leu Pro	
355 360 365	
cct ctt ctt act cct ttc gtt agg tct tgg ctt gat tct ggt tct gat	1151
Pro Leu Leu Thr Pro Phe Val Arg Ser Trp Leu Asp Ser Gly Ser Asp	
370 375 380	
agg ggt ggt gtt aac act gtt act aac tgg caa act gag tct ttc gag	1199
Arg Gly Gly Val Asn Thr Val Thr Asn Trp Gln Thr Glu Ser Phe Glu	
385 390 395	
tct act ctt ggt ctt agg tgc ggt gct ttc act gct agg ggt aac tct	1247
Ser Thr Leu Gly Leu Arg Cys Gly Ala Phe Thr Ala Arg Gly Asn Ser	
400 405 410 415	
aac tac ttc cct gat tac ttc att agg aac att tct ggt gtt cct ctt	1295

Asn Tyr Phe Pro Asp Tyr Phe Ile Arg Asn Ile Ser Gly Val Pro Leu	
420 425 430	
gtt gtt agg aac gag gat ctt agg agg cct ctt cat tac aac gag att	1343
Val Val Arg Asn Glu Asp Leu Arg Arg Pro Leu His Tyr Asn Glu Ile	
435 440 445	
agg aac att gag tct cct tct ggt act cct ggt ggt ctt agg gct tac	1391
Arg Asn Ile Glu Ser Pro Ser Gly Thr Pro Gly Gly Leu Arg Ala Tyr	
450 455 460	
atg gtt tct gtt cat aac agg aag aac aac atc tac gct gtt cat gag	1439
Met Val Ser Val His Asn Arg Lys Asn Asn Ile Tyr Ala Val His Glu	
465 470 475	
aac ggt act atg att cat ctt gct cct gag gat tac acc ggt ttc acc	1487
Asn Gly Thr Met Ile His Leu Ala Pro Glu Asp Tyr Thr Gly Phe Thr	
480 485 490 495	
atc tcc ccc atc cac gcc acc cag gtc aat aat cag acc agg acc ttc	1535
Ile Ser Pro Ile His Ala Thr Gln Val Asn Asn Gln Thr Arg Thr Phe	
500 505 510	
atc tcc gag aag ttc ggc aac cag ggc gac tcc ctg agg ttc gag cag	1583
Ile Ser Glu Lys Phe Gly Asn Gln Gly Asp Ser Leu Arg Phe Glu Gln	
515 520 525	
tcc aac acc acc gcc agg tac acc ctg agg ggc aac ggc aac tcc tac	1631
Ser Asn Thr Thr Ala Arg Tyr Thr Leu Arg Gly Asn Gly Asn Ser Tyr	
530 535 540	
aac ctg tac ctg agg gtg tcc tcc ctg ggc aac tcc acc atc agg gtc	1679
Asn Leu Tyr Leu Arg Val Ser Ser Leu Gly Asn Ser Thr Ile Arg Val	
545 550 555	
acc atc aac ggc agg gtg tac acc gcc tcc aac gtg aac acc acc acc	1727
Thr Ile Asn Gly Arg Val Tyr Thr Ala Ser Asn Val Asn Thr Thr Thr	
560 565 570 575	
aac aac gac ggc gtc aac gac aac ggc gct agg ttc ctg gac atc aac	1775
Asn Asn Asp Gly Val Asn Asp Asn Gly Ala Arg Phe Leu Asp Ile Asn	
580 585 590	
atg ggc aac gtc gtg gcc tcc gac aac acc aac gtg ccc ctg gac atc	1823
Met Gly Asn Val Val Ala Ser Asp Asn Thr Asn Val Pro Leu Asp Ile	
595 600 605	
aac gtg aca ttt aac tcc ggc acc cag ttc gag ctg atg aac atc atg	1871
Asn Val Thr Phe Asn Ser Gly Thr Gln Phe Glu Leu Met Asn Ile Met	
610 615 620	
ttc gtg cca act aac ctg cca ccc atc tac tgagctagc	1910
Phe Val Pro Thr Asn Leu Pro Pro Ile Tyr	
625 630	

<210> 8
 <211> 633
 <212> PRT
 <213> Unknown

<220>

<223> Artificial Sequence

<400> 8

Met Ala Asn Asn Val Leu Asn Asn Gly Arg Thr Thr Ile Cys Asp Ala
1 5 10 15

Tyr Asn Val Val Ala His Asp Pro Phe Ser Phe Glu His Lys Ser Leu
20 25 30

Asp Thr Ile Arg Lys Glu Trp Met Glu Trp Lys Arg Thr Asp His Ser
35 40 45

Leu Tyr Val Ala Pro Ile Val Gly Thr Val Ser Ser Phe Leu Leu Lys
50 55 60

Lys Val Gly Ser Leu Ile Gly Lys Arg Ile Leu Ser Glu Leu Trp Gly
65 70 75 80

Leu Ile Phe Pro Ser Gly Ser Thr Asn Leu Met Gln Asp Ile Leu Arg
85 90 95

Glu Thr Glu Gln Phe Leu Asn Gln Arg Leu Asn Thr Asp Thr Leu Ala
100 105 110

Arg Val Asn Ala Glu Leu Glu Gly Leu Gln Ala Asn Ile Arg Glu Phe
115 120 125

Asn Gln Gln Val Asp Asn Phe Leu Asn Pro Thr Gln Asn Pro Val Pro
130 135 140

Leu Ser Ile Thr Ser Ser Val Asn Thr Met Gln Gln Leu Phe Leu Asn
145 150 155 160

Arg Leu Pro Gln Phe Arg Val Gln Gly Tyr Gln Leu Leu Leu Leu Pro
165 170 175

Leu Phe Ala Gln Ala Ala Asn Met His Leu Ser Phe Ile Arg Asp Val
180 185 190

Val Leu Asn Ala Asp Glu Trp Gly Ile Ser Ala Ala Thr Leu Arg Thr
195 200 205

Tyr Gln Asn Tyr Leu Lys Asn Tyr Thr Thr Glu Tyr Ser Asn Tyr Cys
210 215 220

Ile Asn Thr Tyr Gln Thr Ala Phe Arg Gly Leu Asn Thr Arg Leu His
225 230 235 240

Asp Met Leu Glu Phe Arg Thr Tyr Met Phe Leu Asn Val Phe Glu Tyr
245 250 255

Val Ser Ile Trp Ser Leu Phe Lys Tyr Gln Ser Leu Leu Val Ser Ser
260 265 270

Gly Ala Asn Leu Tyr Ala Ser Gly Ser Gly Pro Gln Gln Thr Gln Ser
275 280 285

Phe Thr Ser Gln Asp Trp Pro Phe Leu Tyr Ser Leu Phe Gln Val Asn
290 295 300

Ser Asn Tyr Val Leu Asn Gly Phe Ser Gly Ala Arg Leu Thr Gln Thr
305 310 315 320

Phe Pro Asn Ile Gly Gly Leu Pro Gly Thr Thr Thr Thr His Ala Leu
325 330 335

Leu Ala Ala Arg Val Asn Tyr Ser Gly Gly Val Ser Ser Gly Asp Ile
340 345 350

Gly Ala Val Phe Asn Gln Asn Phe Ser Cys Ser Thr Phe Leu Pro Pro
355 360 365

Leu Leu Thr Pro Phe Val Arg Ser Trp Leu Asp Ser Gly Ser Asp Arg
370 375 380

Gly Gly Val Asn Thr Val Thr Asn Trp Gln Thr Glu Ser Phe Glu Ser
385 390 395 400

Thr Leu Gly Leu Arg Cys Gly Ala Phe Thr Ala Arg Gly Asn Ser Asn
405 410 415

Tyr Phe Pro Asp Tyr Phe Ile Arg Asn Ile Ser Gly Val Pro Leu Val
420 425 430

Val Arg Asn Glu Asp Leu Arg Arg Pro Leu His Tyr Asn Glu Ile Arg
435 440 445

Asn Ile Glu Ser Pro Ser Gly Thr Pro Gly Gly Leu Arg Ala Tyr Met
450 455 460

Val Ser Val His Asn Arg Lys Asn Asn Ile Tyr Ala Val His Glu Asn

465		470		475		480
Gly Thr Met Ile His Leu Ala Pro Glu Asp Tyr Thr Gly Phe Thr Ile						
	485			490		495
Ser Pro Ile His Ala Thr Gln Val Asn Asn Gln Thr Arg Thr Phe Ile						
	500			505		510
Ser Glu Lys Phe Gly Asn Gln Gly Asp Ser Leu Arg Phe Glu Gln Ser						
	515			520		525
Asn Thr Thr Ala Arg Tyr Thr Leu Arg Gly Asn Gly Asn Ser Tyr Asn						
	530			535		540
Leu Tyr Leu Arg Val Ser Ser Leu Gly Asn Ser Thr Ile Arg Val Thr						
	545			550		555
						560
Ile Asn Gly Arg Val Tyr Thr Ala Ser Asn Val Asn Thr Thr Thr Asn						
	565			570		575
Asn Asp Gly Val Asn Asp Asn Gly Ala Arg Phe Leu Asp Ile Asn Met						
	580			585		590
Gly Asn Val Val Ala Ser Asp Asn Thr Asn Val Pro Leu Asp Ile Asn						
	595			600		605
Val Thr Phe Asn Ser Gly Thr Gln Phe Glu Leu Met Asn Ile Met Phe						
	610			615		620
Val Pro Thr Asn Leu Pro Pro Ile Tyr						
	625			630		

<210> 9
 <211> 1910
 <212> DNA
 <213> Unknown

<220>

<223> artificial cry2Ae DNA sequence for expression in corn

<400> 9

ccatggctaa caacgtgctg aacaacggca ggaccacat ctgcgatgca tacaacgtgg	60
tggcccacga cccattcagc ttcgagcaca agagcctgga caccatccgc aaggagtgga	120
tggagtggaa gcgcaccgac cacagcctgt acgtggcccc tatcgtgggc accgtgagca	180
gcttcttgct gaagaagggtg ggcagcctga tcggcaagag gatcctgagc gagctgtggg	240
gcctgatctt cccaagcggc agcaccaacc tgatgcagga catcctgagg gagaccgagc	300

agttcctgaa ccagcgctg aacaccgaca ccctggctcg cgtgaacgcc gagctggagg	360
gcctccaggc caacatcagg gaattcaacc agcaggtgga caacttcctg aaccaacccc	420
agaacccagt gccactgagc atcaccagca gcgtgaacac catgcagcag ctgttcctga	480
accgctgcc acagttccgc gtgcagggct accagctgct gctgctgcca ctgttcgccc	540
aggctgccaa catgcaccta agcttcaccc gcgacgtggc gctgaacgcc gacgagtggg	600
gcacagcgc tgccaccctg cgcacctacc agaactacct gaagaactac accaccgagt	660
acagcaacta ctgcatcaac acctaccaga ccgccttcag gggcctgaac accaggctgc	720
acgacatgct ggagttccgc acctacatgt tcctgaacgt gtgcgagtac gtgagcatct	780
ggagcctggt caagtaccag agcctgctgg tgagcagcgg tgccaacctg tacgccagcg	840
gcagcggctc acagcagacc cagagcttca ccagccagga ctggcccttc ctgtacagcc	900
tggtccaggt gaacagcaac tacgtgctga acggcttcag cgggtgccagg ctgacctaga	960
ccttcccaaa catcggaggc ctgccaggca ccaccaccac ccacgcctg ctggctgcca	1020
gggtgaacta cagcgggtggc gtgagcagcg gcgatatcgg cgtgtgttc aaccagaact	1080
tcagctgcag caccttcctg ccaccactgc tgacccatt cgtgcgcagc tggctggaca	1140
gcggcagcga caggggtggc gtgaacaccg tgaccaactg gcagaccgag agcttcgaga	1200
gcaccctggg cctgcgctgc ggtgccttca ccgccagggg caacagcaac tacttcccag	1260
actacttcat ccgcaacatc agcggcgtgc cactgggtggc gcgcaacgag gacctgcga	1320
ggccactgca ctacaacgag atccgcaaca tcgagagccc aagcggcacc ccaggaggcc	1380
tgagggccta catggtgagc gtgcacaacc gcaagaacaa catctacgcc gtgcacgaga	1440
acggcaccat gatccacctg gcccagagg actacaccgg ttccaccatc tccccatcc	1500
acgccacca ggtcaataat cagaccagga ccttcatttc cgagaagttc ggcaaccagg	1560
gcgactccct gaggttcgag cagtccaaca ccaccgccag gtacaccctg aggggcaacg	1620
gcaactccta caacctgtac ctgagggtgt cctccctcgg caactccacc atcagggtca	1680
ccatcaacgg caggggtgtac accgcctcca acgtgaacac caccaccaac aacgacggcg	1740
tcaacgacaa cggcgctagg ttcttgga tcaacatggg caacgtcgtg gcctccgaca	1800
acaccaacgt gccctggac atcaacgtga catttaactc cggcaccag ttcgagctga	1860
tgaacatcat gtgcgtgcca actaacctcc caccatcta ctgagctagc	1910